

Hayes, Robert

1817

#18

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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,594A**

DATE: 08/18/97  
TIME: 14:34:46

**INPUT SET: S19735.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

## **SEQUENCE LISTING**

1  
2  
3 (1) General Information:

5 (i) APPLICANT: O'Brien, John S.  
6 Kishimoto, Yasuo

8 (ii) TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES  
9 DERIVED THEREFROM

(iii) NUMBER OF SEQUENCES: 11

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Knobbe, Martens, Olson and Bear  
15 (B) STREET: 620 Newport Center Drive, Sixteenth Floor  
16 (C) CITY: Newport Beach  
17 (D) STATE: CA  
18 (E) COUNTRY: USA  
19 (F) ZIP: 92660

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette  
23 (B) COMPUTER: IBM Compatible  
24 (C) OPERATING SYSTEM: DOS  
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0

27 (vi) CURRENT APPLICATION DATA:

28 (A) APPLICATION NUMBER: 08/484,594  
29 (B) FILING DATE: 07-JUN-1995  
30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/100,247  
34 (B) FILING DATE: 30-JUL-1993

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Israelsen, Ned A  
38 (B) REGISTRATION NUMBER: 29,655  
39 (C) REFERENCE/DOCKET NUMBER: MYELOS.002DV2

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 619-235-8550  
43 (B) TELEFAX: 619-235-0176  
44 (C) TELEX:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/484,594ADATE: 08/18/97  
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47 (2) INFORMATION FOR SEQ ID NO:1:  
4849 (i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 22 amino acids  
51 (B) TYPE: amino acid  
52 (C) STRANDEDNESS: single  
53 (D) TOPOLOGY: linear54  
55 (ii) MOLECULE TYPE: peptide  
56 (v) FRAGMENT TYPE: internal

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

58 Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys  
59 1 5 10 15  
60 Thr Glu Lys Glu Ile Leu  
61 20  
6263 (2) INFORMATION FOR SEQ ID NO:2:  
6465 (i) SEQUENCE CHARACTERISTICS:  
66 (A) LENGTH: 523 amino acids  
67 (B) TYPE: amino acid  
68 (C) STRANDEDNESS: single  
69 (D) TOPOLOGY: linear70 (ii) MOLECULE TYPE: peptide  
71 (v) FRAGMENT TYPE: N-terminal72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
7374 Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala  
75 1 5 10 15  
76 Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp  
77 20 25 30  
78 Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys  
79 35 40 45  
80 Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp  
81 50 55 60  
82 Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn  
83 65 70 75 80  
84 Ala Thr Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp  
85 85 90 95  
86 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser  
87 100 105 110  
88 Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro  
89 115 120 125  
90 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His  
91 130 135 140  
92 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro  
93 145 150 155 160  
94 Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro  
95 165 170 175  
96

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100 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys  
101 180 185 190  
102 Asp Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile Gln  
103 195 200 205  
104 Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu His  
105 210 215 220  
106 Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile Cys  
107 225 230 235 240  
108 Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met  
109 245 250 255  
110 His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp Glu  
111 260 265 270  
112 Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala Ser  
113 275 280 285  
114 Lys Asn Val Ile Pro Ala Leu Asp Leu Val Asp Pro Ile Lys Lys His  
115 290 295 300  
116 Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu  
117 305 310 315 320  
118 Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu  
119 325 330 335  
120 Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu  
121 340 345 350  
122 Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu  
123 355 360 365  
124 Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu  
125 370 375 380  
126 His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val Thr  
127 385 390 395 400  
128 Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val Gly  
129 405 410 415  
130 Thr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile Leu  
131 420 425 430  
132 Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln Lys  
133 435 440 445  
134 Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu Ile  
135 450 455 460  
136 Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly Ala  
137 465 470 475 480  
138 Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile Trp  
139 485 490 495  
140 Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys Asn  
141 500 505 510  
142 Ala Val Glu His Cys Lys Arg His Val Trp Asn  
143 515 520  
144  
145 (2) INFORMATION FOR SEQ ID NO:3:  
146  
147 (i) SEQUENCE CHARACTERISTICS:  
148 (A) LENGTH: 80 amino acids  
149 (B) TYPE: amino acid  
150 (C) STRANDEDNESS: single  
151 (D) TOPOLOGY: linear  
152

**RAW SEQUENCE LISTING  
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153           (ii) MOLECULE TYPE: protein  
 154           (v) FRAGMENT TYPE: internal  
 155  
 156           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
 157  
 158       Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr  
 159                1                       5                       10                       15  
 160       Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe  
 161                20                      25                       30  
 162       Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln  
 163                35                      40                       45  
 164       Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu  
 165                50                      55                       60  
 166       Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly  
 167                65                      70                       75                       80  
 168  
 169           (2) INFORMATION FOR SEQ ID NO:4:  
 170  
 171           (i) SEQUENCE CHARACTERISTICS:  
 172            (A) LENGTH: 2740 base pairs  
 173            (B) TYPE: nucleic acid  
 174            (C) STRANDEDNESS: single  
 175            (D) TOPOLOGY: linear  
 176  
 177           (ii) MOLECULE TYPE: cDNA  
 178  
 179           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
 180  
 181       ATGTACGCCCT TCTTCCTCCTT GGCCAGCCTC CTGGGGCGGG CTCTAGCCGG CCCGGTCCTT       60  
 182       GGACTGAAAG AATGCACCAAG GGGCTCGGCA GTGTGGTGCC AGAATGTGAA GACGGCGTCC       120  
 183       GACTGCAGGG CAGTGAAGCA CTGCCTGCAG ACCGTTGGA ACAAGCCAAC ACTGAAATCC       180  
 184       CTTCCCTGCG ACATATGCAA AGACGTTGTC ACCGCAGCTG GTGATATGCT GAAGGACAAT       240  
 185       GCCACTGAGG AGGAGATCCT TGTTTACTTG GAGAAGACCT GTGACTGGCT TCCGAAACCG       300  
 186       AACATGTCTG CTTCATGCAA GGAGATAGTG GACTCCCTACC TCCTGTCTCAT CCTGGACATC       360  
 187       ATTAAAGGAG AAATGAGCCG TCCTGGGGAG GTGTGCTCTG CTCTCAACCT CTGCGAGTCT       420  
 188       CTCCAGAACG ACCTAGCAGA GCTGAATCAC CAGAAGCAGC TGGAGTCCAA TAAGATCCCA       480  
 189       GAGCTGGACA TGACTGAGGT GGTGGCCCCC TTCACTGGCCA ACATCCCTCT CCTCCTCTAC       540  
 190       CCTCAGGACG GCCCCCGCAG CAAGCCCCAG CCAAAGGATA ATGGGGACGT TTGCCAGGAC       600  
 191       TGCATTCAAGA TGGTGACTGA CATCCAGACT GCTGTACGGA CCAAATCCAC CTTTGTCCAG       660  
 192       GCCTTGGTGG AACATGTCAA GGAGGAGTGT GACCGCCTGG GCCCTGGCAT GGCCGACATA       720  
 193       TGCAAGAACT ATATCAGCCA GTATTCTGAA ATTGCTATCC AGATGATGAT GCACATGCAA       780  
 194       CCCAAGGAGA TCTGTGGCT GGTGGGGTTC TGTGATGAGG TGAAAGAGAT GCCCCATGCAG       840  
 195       ACTCTGGTCC CCGCCAAAGT GGCCTCCAAG AATGTCATCC CTGCCCCTGGA ACTGGTGGAG       900  
 196       CCCATTAAAGA AGCACGAGGT CCCAGCAAAG TCTGATGTTT ACTGTGAGGT GTGTGAATTG       960  
 197       CTGGTGAAGG AGGTGACCAA GCTGATTGAC AACACAAGA CTGAGAAAGA AATAACTCGAC       1020  
 198       GCTTTGACA AAATGTGCTC GAAGCTGCCG AAGTCCCTGT CGGAAGAGTG CCAGGAGGTG       1080  
 199       GTGGACACGT ACGGCAGCTC CATCCTGTCC ATCCTGCTGG AGAGGAGTCAG CCCTGAGCTG       1140  
 200       GTGTGCAGCA TGCTGCACCT CTGCTCTGGC ACGCGGCTGC CTGCACTGAC CGTTCACGTG       1200  
 201       ACTCAGCCAA AGGACGGTGG CTTCTGCGAA GTGTGCAAGA AGCTGGTGGG TTATTGATGAT       1260  
 202       CGAACCTGG AGAAAAACAG CACCAAGCAG GAGATCCTGG CTGCTCTTGA GAAAGGCTGC       1320  
 203       AGCTTCCTGC CAGACCCCTTA CCAGAAGCAG TGTGATCAGT TTGTGGCAGA GTACGAGCCC       1380  
 204       GTGCTGATCG AGATCCTGGT GGAGGTGATG GATCCTCCT TCGTGTGCTT GAAAATTGGA       1440  
 205       GCCTGCCCCCT CGGCCCCATAA GCCCTTGTG GGAAGTGTGAGA AGTGTATATG GGGCCCAAGC       1500

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206	TACTGGTGCC	AGAACACAGA	GACAGCAGCC	CAGTGCATG	CTGTCGAGCA	TTGCAAACGC	1560
207	CATGTGTGGA	ACTAGGAGGA	GGAAATATTCC	ATCTTGGCAG	AAACCACAGC	ATTGGTTTTT	1620
208	TTCTACTTGT	GTGTCTGGGG	GAATGAACGC	ACAGATCTGT	TTGACTTTGT	TATAAAAATA	1680
209	GGGCTCCCCC	ACCTCCCCCA	TTTCTGTGTC	CTTTATTGTA	GCATTGCTGT	CTGCAAGGGA	1740
210	GCCCCTAGCC	CCTGGCAGAC	ATAGCTGCTT	CAGTGCCCT	TTTCTCTCTG	CTAGATGGAT	1800
211	GTTGATGCAC	TGGAGGTCTT	TTAGCCTGCC	CTTGCATGGC	GCCTGCTGGA	GGAGGAGAGA	1860
212	GCTCTGCTGG	CATGAGCCAC	AGTTTCTTGA	CTGGAGGCCA	TCAACCCCTCT	TGGTTGAGGC	1920
213	CTTGTCTGA	GCCCTGACAT	GTGCTTGGGC	ACTGGTGGGC	CTGGGCTTCT	GAGGTGGCCT	1980
214	CCTGCCCTGA	TCAGGGACCC	TCCCCGCTTT	CCTGGGCCCTC	TCAGTTGAAC	AAAGCAGCAA	2040
215	AACAAAGGCA	GTTTTATATG	AAAGATTAGA	AGCCTGGAAT	AATCAGGCTT	TTTAAATGAT	2100
216	GTAATTCCCA	CTGTAATAGC	ATAGGGATTT	TGGAAGCAGC	TGCTGGTGGC	TTGGGACATC	2160
217	AGTGGGGCCA	AGGGTTCTCT	GTCCCCTGGTT	CAACTGTGAT	TTGGCTTTCC	CGTGTCTTTC	2220
218	CTGGTGTGTC	CTTGTGTTGGG	GTTCTGTGGG	TTTGGGTGGG	AAGAGGGCAA	TCTGCCTGAA	2280
219	TGTAACCTGC	TAGCTCTCCG	AAGGCCCTGC	GGGCCTGGCT	TGTGTGAGCG	TGTGGACAGT	2340
220	GGTGGCCGCG	CTGTGCCCTGC	TCGTGTTGCC	TACATGTCCC	TGGCTGTTGA	GGCGCTGCTT	2400
221	CAGCCTGCAC	CCCTCCCCCTG	TCTCATAGAT	GCTCCTTTG	ACCTTTTCAA	ATAAAATATGG	2460
222	ATGGCGAGCT	CCTAGGCCTC	TGGCTTCCTG	GTAGAGGGCG	GCATGCCGAA	GGGTCTGCTG	2520
223	GGTGTGGATT	GGATGCTGGG	GTGTGGGGGT	TGGAAGCTGT	CTGTGGCCCA	CTTGGGCACC	2580
224	CACGCTTCTG	TCCACTTCTG	GTTGCCAGGA	GACAGCAAGC	AAAGCCAGCA	GGACATGAAG	2640
225	TTGCTATTAA	ATGGACTTCG	TGATTTTTGT	TTTGCACTAA	AGTTTCTGTG	ATTTAACAAAT	2700
226	AAAATTCTGT	TAGCCAGAAA	AAAAAAAAAA	AAAAAAAAAA			2740

227

(2) INFORMATION FOR SEQ ID NO:5:

228

229

(i) SEQUENCE CHARACTERISTICS:

230

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

231

(ii) MOLECULE TYPE: peptide

232

(v) FRAGMENT TYPE: internal

233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

234

235

Tyr	Lys	Glu	Va	l	Th	Lys	Leu	Ile	Asp	Asn	Asn	Lys	Thr	Glu	Lys	Glu
1				5						10				15		

236

Ile	Leu
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237

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(2) INFORMATION FOR SEQ ID NO:6:

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(i) SEQUENCE CHARACTERISTICS:

259

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

260

(ii) MOLECULE TYPE: peptide 4

261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

262

Cys	Gln	Phe	Val	Met	Asn	Lys	Phe	Ser	Glu	Leu	Ile	Val	Asn	Asn	Ala
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**SEQUENCE VERIFICATION REPORT  
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Original Text